AMENDMENTS TO THE SPECIFICATION

Kindly amend the specification, without prejudice, without admission, without surrender of subject matter, and without any intention of creating any estoppel as to equivalents, to read as follows:

Please delete the paragraph on page 12, line 26 to page 13, line 7, and replace it with the following paragraph:

Figure 2 shows structure/function analysis of mutations. (A) Sequence alignment of the Mtu intein (middle), other inteins (top) and hedgehog proteins (bottom). Mutation locations of the ΔI-SM and ΔI-CM mutants are indicated relative to conserved intein sequence blocks. Highly conserved residues are white on black, while hydrophobic residues are boxed. **Peptide sequences are shown in SEQ ID NOS 9-26, by column, respectively.** (B) Mutation locations relative to the Mxe *gyrA* intein structure. Mutated residues based on alignments in panel (A) are indicated on the Mxe *gyrA* intein backbone. N and C indicate the N- and C-terminal intein residues. (C) Model for DI-CM mini-intein cleavage. In the wild type, H-bonds or electrostatic interactions (.....) inhibit the C-terminal Asn 441 (N) from succinimide formation until after extein ligation (left). By removing such a bond (drawn here to the terminal Asn but in principle could be to any residue critical for cleavage), the D422G mutant facilitates succinimide formation and C-terminal cleavage (right). In C, C is Cys 1, A is Ala 1 mutant, D is Asp 422, G is Gly 422 mutant, N is Asn 441 and S* is succinimide ring. Figure 2 is discussed in the Specification.

AMENDMENTS TO THE DRAWINGS

Kindly amend the drawings, without prejudice, without admission, without surrender of subject matter, and without any intention of creating any estoppel as to equivalents, to read as follows:

Please delete Figure 2, and replace it with replacement Figure 2.